

Supplementary Figures

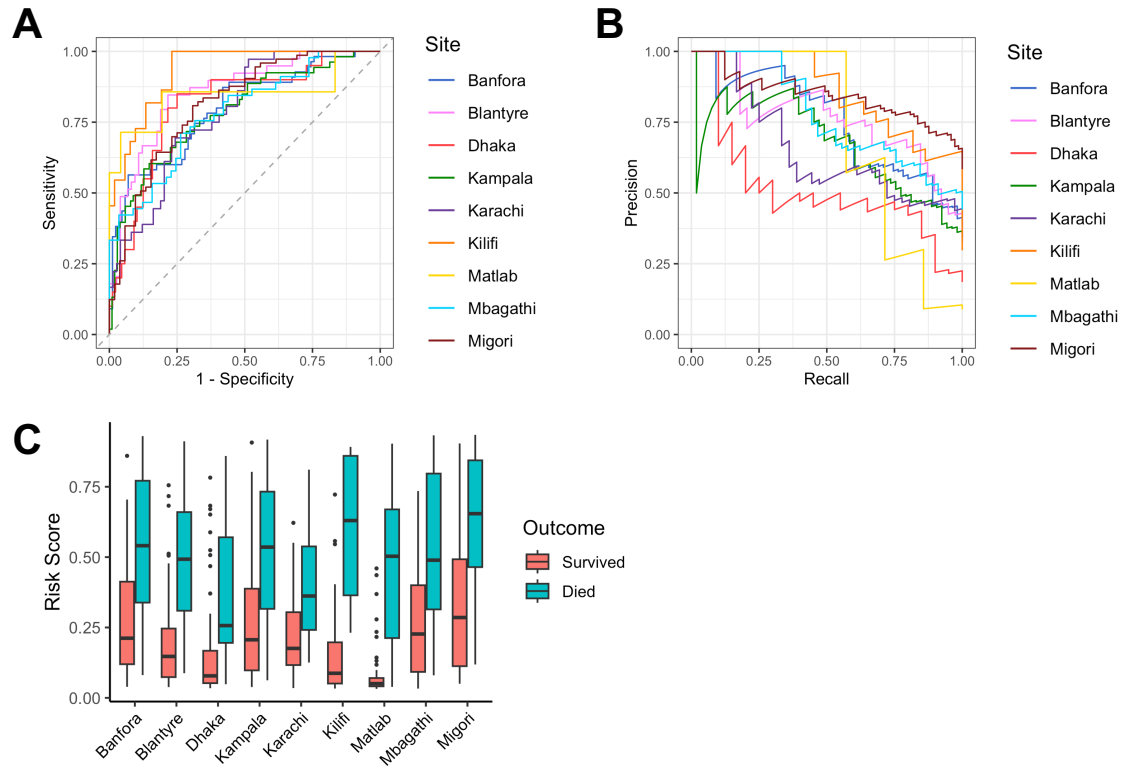


Figure S1. Performance of the multiomic model for the prediction of mortality during hospitalization and post-discharge. A cross-validated XGBoost model for the prediction of mortality during hospitalization or in the post-discharge period was trained on the integrated multiomic data of the discovery cohort. **(A)** ROC curves for the multiomic model stratified by study site. **(B)** Precision-recall curves for the multiomic model stratified by study site. **(C)** Distribution of the mortality risk scores predicted by the multiomic model stratified by patient outcome and study site. Box plots indicate median (middle line); 25th and 75th percentiles (box limits); 1.5*interquartile range (error bars); and outliers (single points).

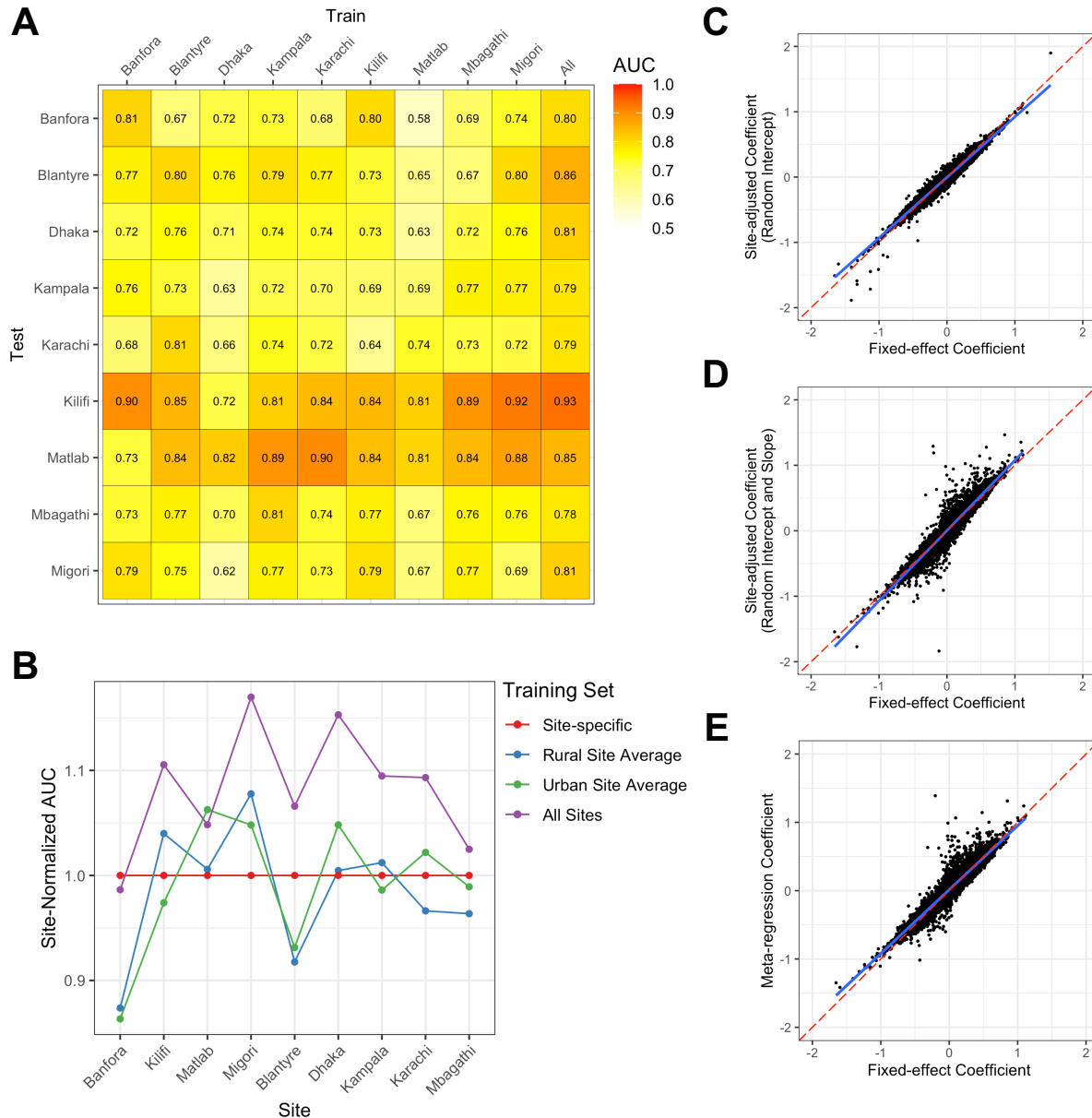


Figure S2. Generalizability of the multiomic signatures of mortality across sites. (A-B) Site-specific cross-validated XGBoost models were built for the prediction of mortality during hospitalization or in the post-discharge period. (A) Classification performance of each site-specific model assessed across every other site using the AUROC. (B) Site-normalized AUROCs for site-specific models applied across every other site and aggregated by urban or rural status. (C-E) Each multiomic feature's association with mortality at hospital admission was quantified with site-unadjusted and site-adjusted logistic regressions. Non-adjusted fixed-effect coefficient estimates are shown compared to site-adjusted coefficient estimates generated with random intercepts (C), random intercepts and random slopes (D), or a meta-regression framework (E). The blue lines and shadows represent the regression lines and the 95% Confidence Intervals, respectively.

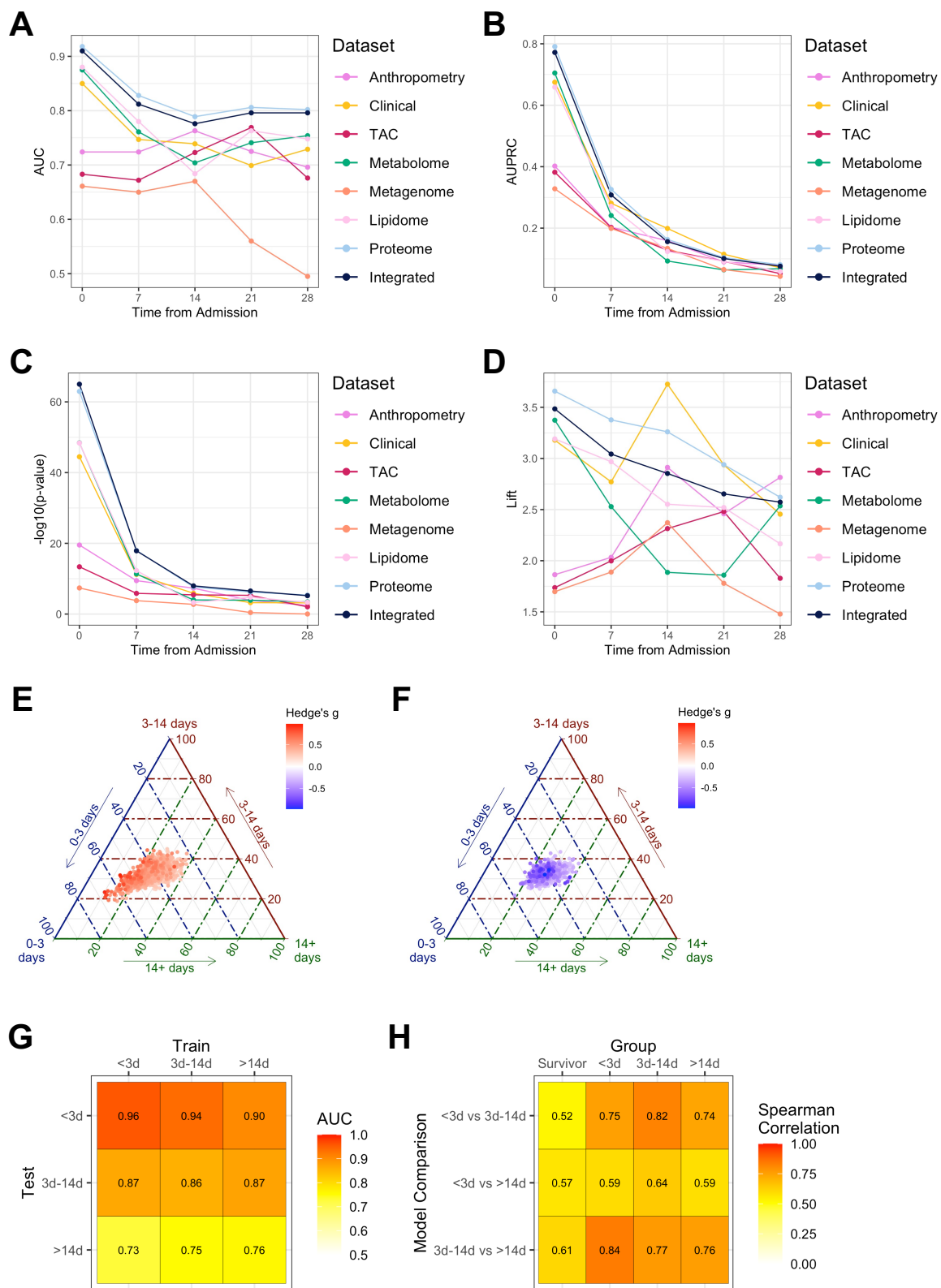


Figure S3. Temporal analysis of the multiomic signature of mortality during hospitalization and post-discharge. (A-D) Cross-validated XGBoost models were built using each dataset separately for the prediction of mortality during hospitalization or in the post-discharge period and their performances assessed using only the cases that occurred in 14-day intervals. AUROCs (A), AUPRCs (B), uncorrected Wilcoxon rank sum test p-values (C), and lifts (prevalence-adjusted AUPRCs, D) of the models built on each dataset evaluated on 14-day intervals. (E-F) The hedge's g for each feature's association with mortality or survival at hospital admission was calculated using only cases that died in the specified timeframe. Ternary plots depicting each timeframe's relative hedge's g for each feature significantly associated with mortality (E) or survival (F) with at least a small effect size ($|\text{hedge's } g| > 0.2$). (G-H) Cross-validated XGBoost models for the prediction of mortality during hospitalization or in the post-discharge period were built using only the cases that occurred in the specified timeframes. Models were then tested with the cases from the other timeframes (G) and model predictions between models compared (H).

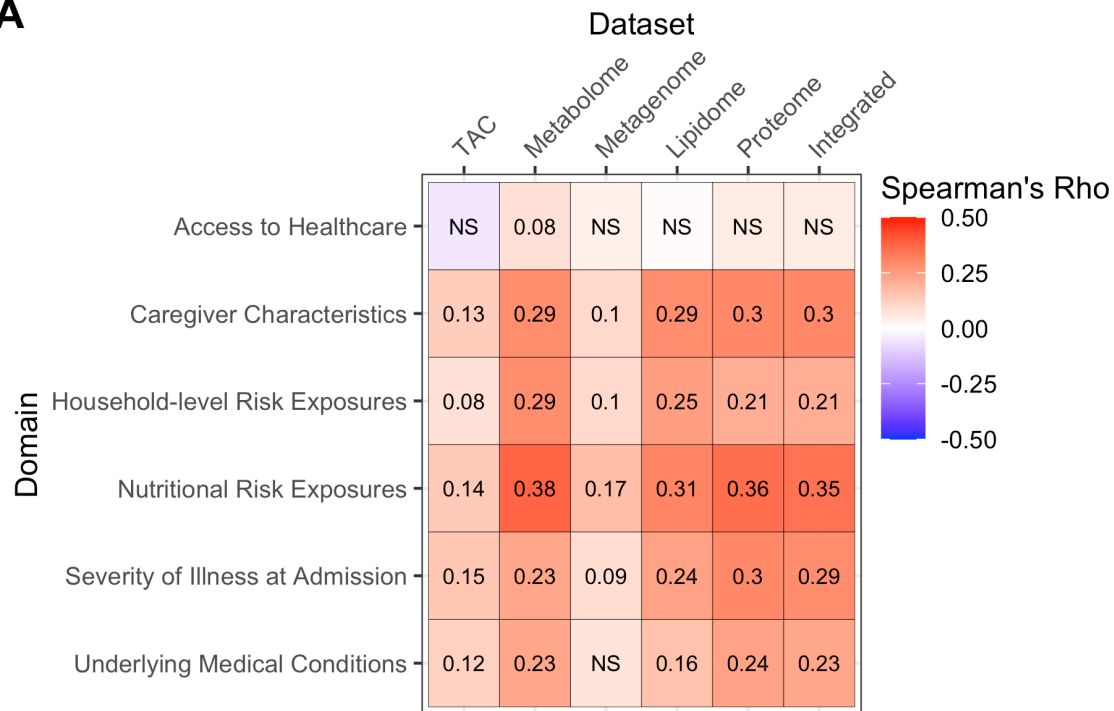
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Figure S4. Association of the multiomic signatures of mortality and immediate and underlying domains of exposure. Cross-validated XGBoost models were built using each dataset separately for the prediction of mortality during hospitalization or in the post-discharge period. Immediate and underlying exposure variables influencing mortality risk were grouped into domains to generate latent factors capturing overall exposure effects. (A) Heatmap showing the Pearson correlation of the different omic signatures of mortality with different domains of exposure. NS = Not Significant.

A

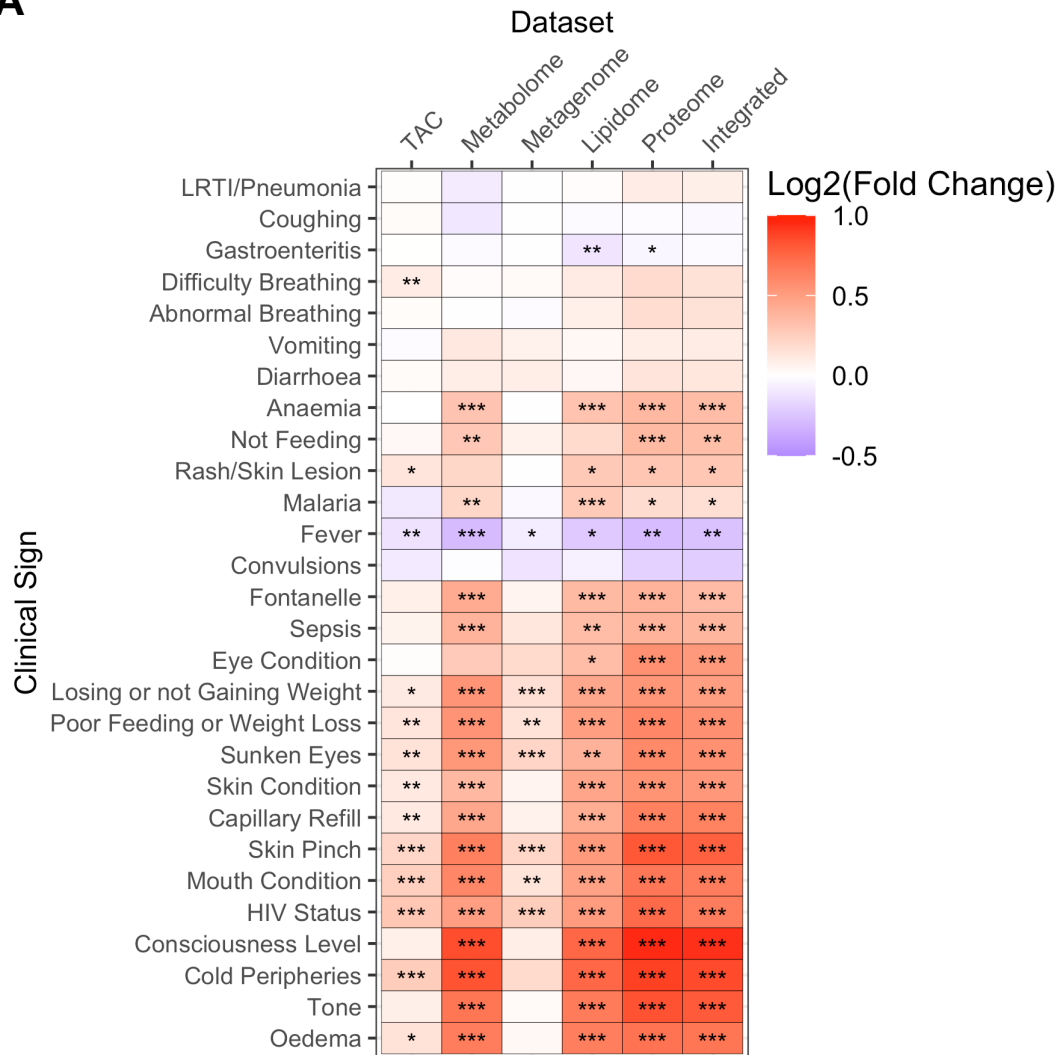


Figure S5. Association of the multiomic signatures of mortality and clinical signs of disease at admission. Cross-validated XGBoost models were built using each dataset separately for the prediction of mortality during hospitalization or in the post-discharge period. (A) Heatmap showing the association of the different omic signatures of mortality with different clinical signs of disease. Asterisks indicate statistical significance assessed with a two-tailed Wilcoxon rank sum test and corrected for multiple hypothesis testing: * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.

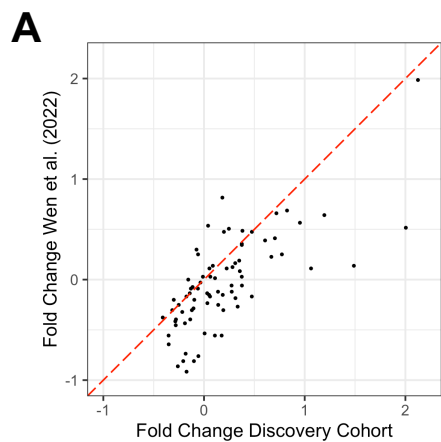


Figure S6. Validation of the metabolomic signature of mortality with the F75 study. Metabolites between studies were matched using Human Metabolome Database IDs. The association with mortality of each matched metabolite was assessed in the discovery cohort using log fold change. **(A)** Comparison of the association of each metabolite with mortality in the discovery cohort and the previously-published metabolomic results from the F75 study.

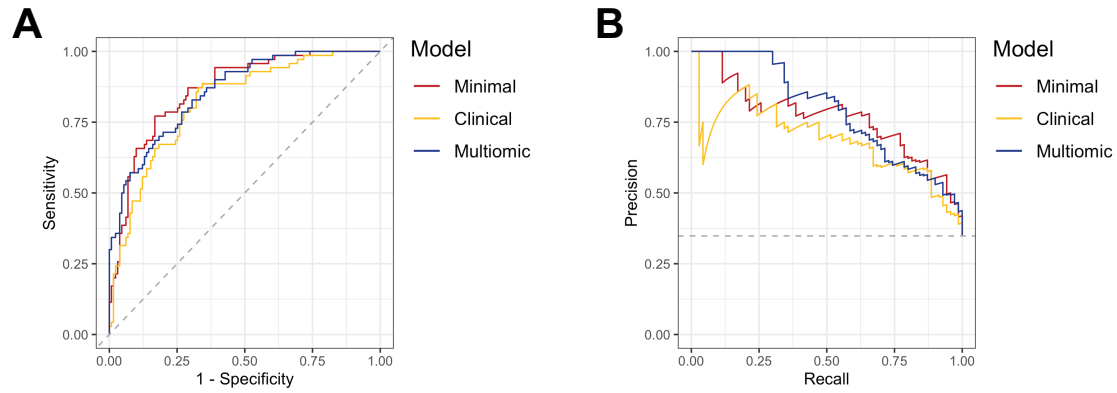


Figure S7. Performance of the minimal model for the prediction of mortality during hospitalization and post-discharge. Participants were randomly split into a training set ($N = 807$, 80%) and a test set ($N = 201$, 20%) to build a minimal XGBoost model for the prediction of mortality. ROC (A) and precision-recall (B) curves for the minimal, multiomic, and clinical models.

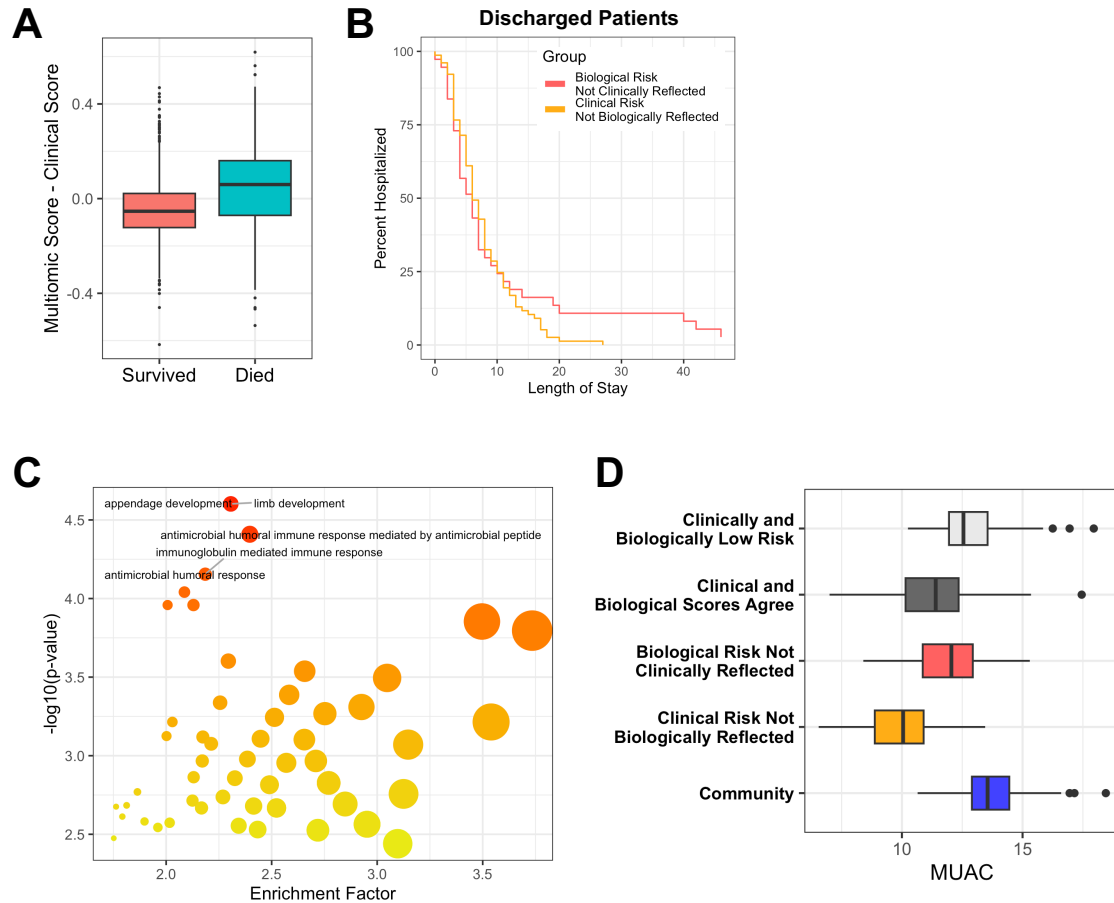


Figure S8. Characterization of the patient subgroups with discrepant clinical and multiomic mortality risk scores at hospital admission. (A) The differences between the mortality risk scores predicted by the multiomic model and the clinical model described in **Figure 2B** stratified by patient outcome ($N = 965$). (B-D) Cross-validated XGBoost models for the prediction of mortality during hospitalization or in the post-discharge period were trained on the clinical data and the integrated multiomic data for the subset of discovery cohort members with all omics datasets available ($N = 629$). (B) Kaplan-Meier curve for the discrepant subgroups defined in **Figure 3A** showing the length of hospital stay for all discharged patients. (C) GO overrepresentation analysis performed on the plasma proteome between the discrepant subgroups defined in **Figure 3A**. Plot shows uncorrected two-sided p-values obtained using Fisher's exact test. (D) Distribution of patient MUACs stratified by the patient subgroups defined in **Figure 3A**. Box plots indicate median (middle line); 25th and 75th percentiles (box limits); 1.5*interquartile range (error bars); and outliers (single points).

A

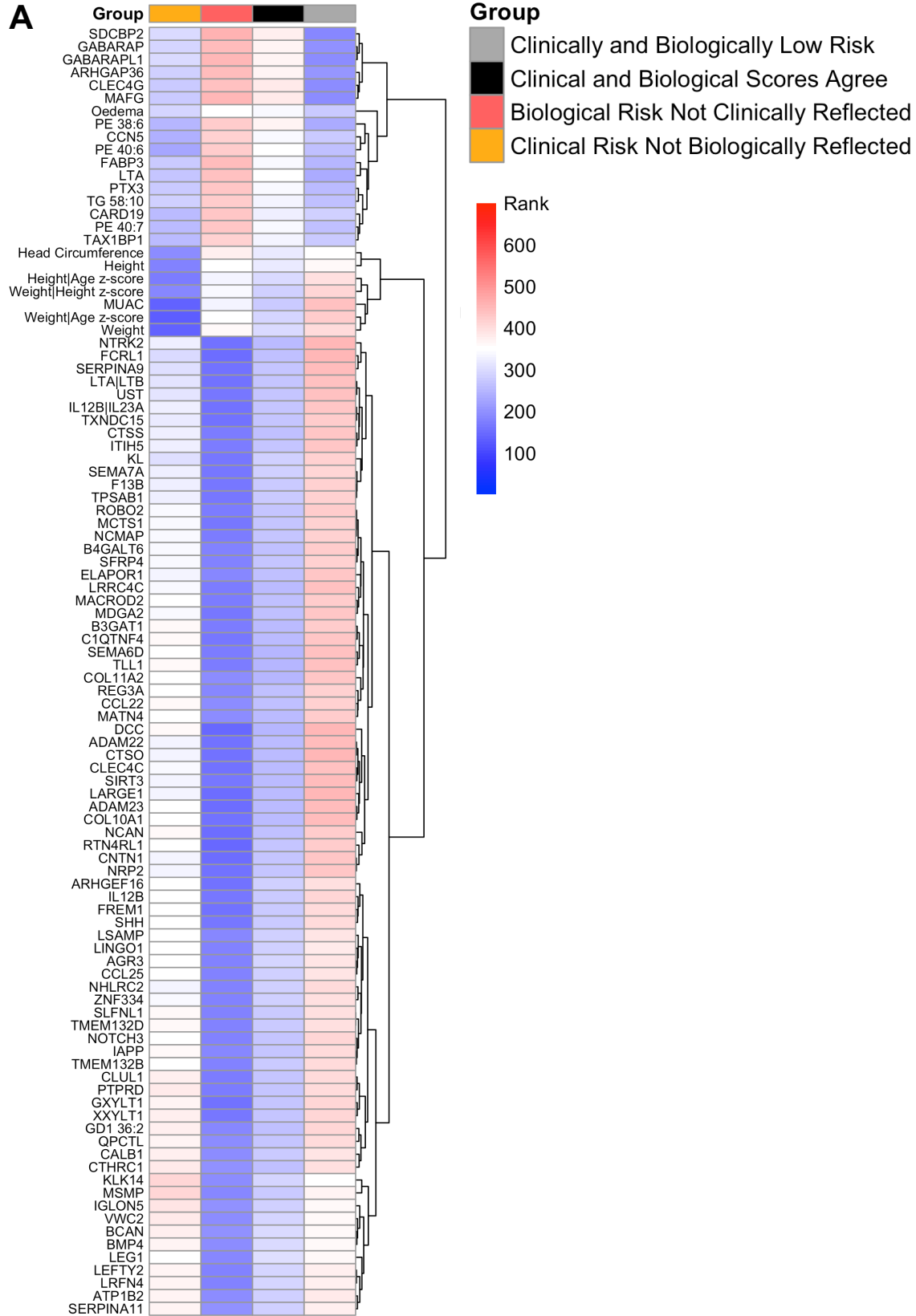


Figure S9. Contrasting features of the patient subgroups with discrepant clinical and multiomic mortality risk scores at hospital admission. Cross-validated XGBoost models for the prediction of mortality during hospitalization or in the post-discharge period were trained on the clinical data and the integrated multiomic data for the subset of discovery cohort members with all omics datasets available ($N = 629$). (A) Heatmap of the clinical and multiomic features most different between the discrepant subgroups defined in **Figure 3A**.

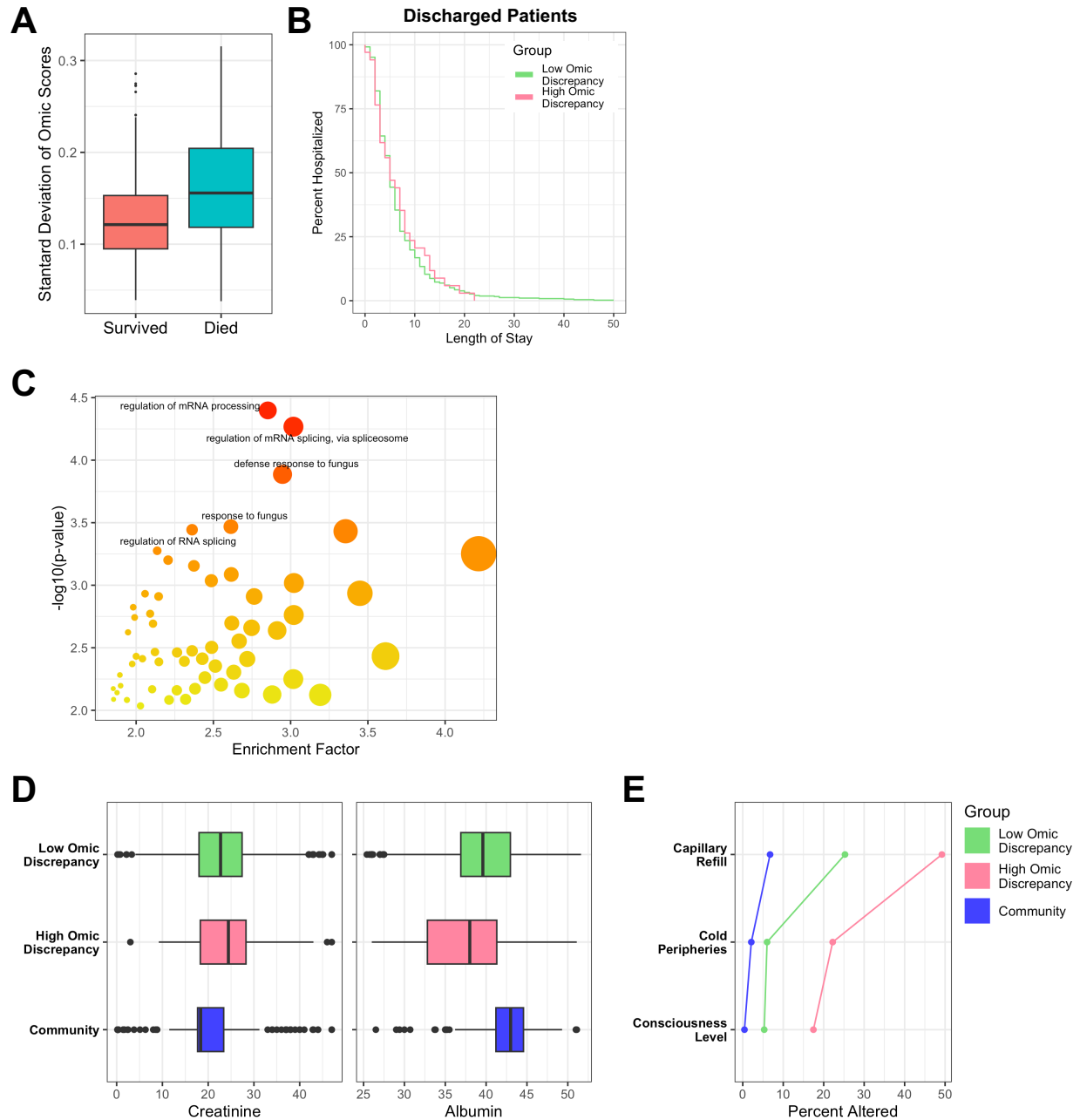


Figure S10. Characterization of the patient subgroups with discrepant interomic mortality risk scores at hospital admission. (A) Multiomic discrepancy scores of the models in **Figure 2B** stratified by patient outcome ($N = 629$). (B-E) Cross-validated XGBoost models for the prediction of mortality during hospitalization or in the post-discharge period were trained on each omic dataset for the subset of discovery cohort members with all omics datasets available ($N = 629$). (B) Kaplan-Meier curve for the discrepant subgroups defined in **Figure 3E** showing the length of hospital stay for all discharged patients. (C) GO overrepresentation analysis performed on the plasma proteome between the discrepant subgroups defined in **Figure 3E**. Plot shows uncorrected two-sided p-values obtained using Fisher's exact test. (D) Distribution of

patient creatinine and albumin levels stratified by the patient subgroups defined in **Figure 3E**. (E) Percentage of patients with altered clinical assessments stratified by the patient subgroups defined in **Figure 3E**. Box plots indicate median (middle line); 25th and 75th percentiles (box limits); 1.5*interquartile range (error bars); and outliers (single points).

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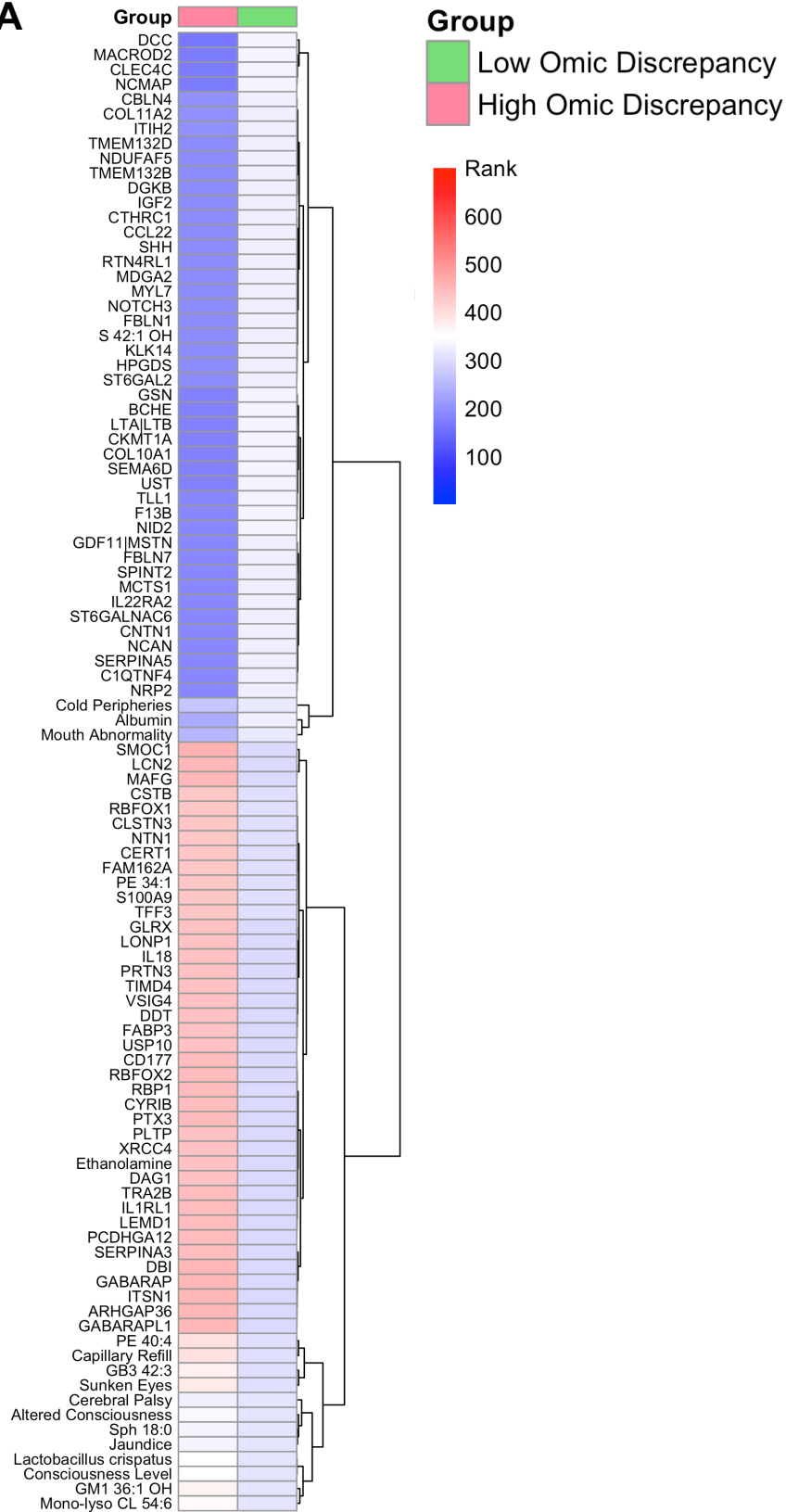


Figure S11. Contrasting features of the patient subgroups with discrepant interomic mortality risk scores at hospital admission. Cross-validated XGBoost models for the prediction of mortality during hospitalization or in the post-discharge period were trained on each omic dataset for the subset of discovery cohort members with all omics datasets available ($N = 629$). **(A)** Heatmap of the clinical and multiomic features most different between the discrepant subgroups defined in **Figure 3E**.

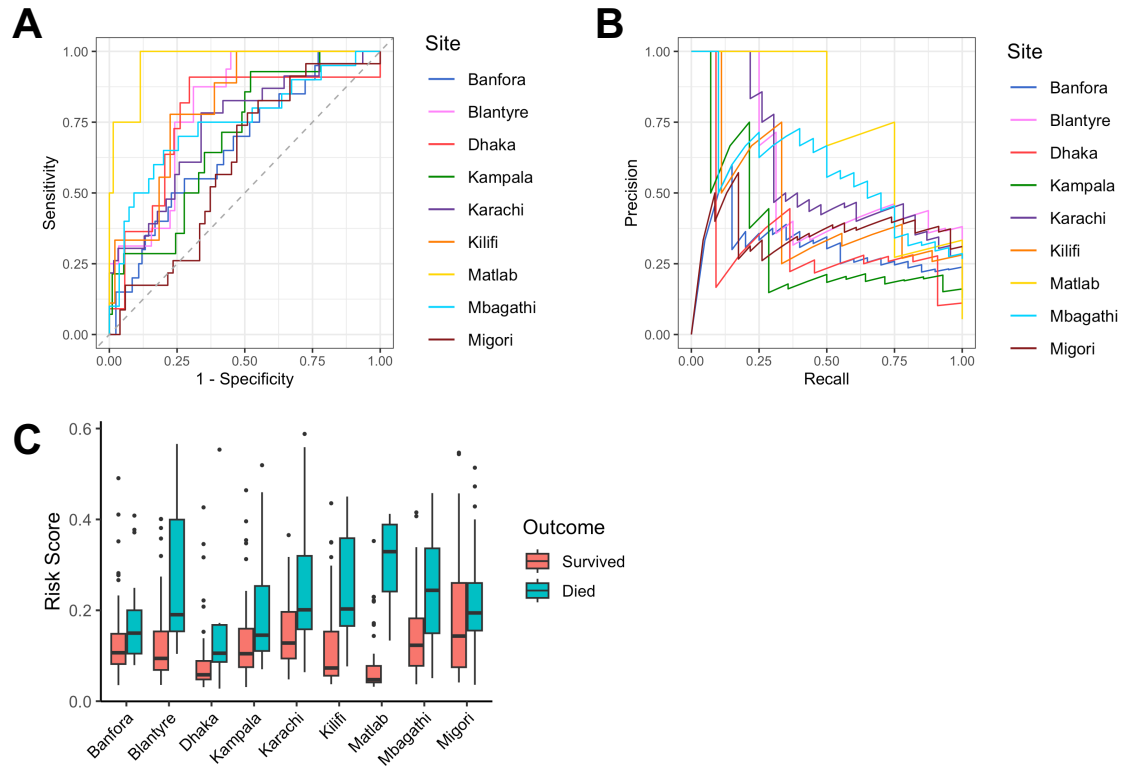


Figure S12. Site-specific analysis of the multiomic model for the prediction of mortality in the post-discharge period. A cross-validated XGBoost model for the prediction of mortality in the post-discharge period was trained on the integrated multiomic data of the discovery cohort. **(A)** ROC curves for the multiomic model stratified by site of origin. **(B)** Precision-recall curves for the multiomic model stratified by site of origin. **(C)** Distribution of the mortality risk scores predicted by the multiomic model stratified by patient outcome and site of origin. Box plots indicate median (middle line); 25th and 75th percentiles (box limits); 1.5*interquartile range (error bars); and outliers (single points).

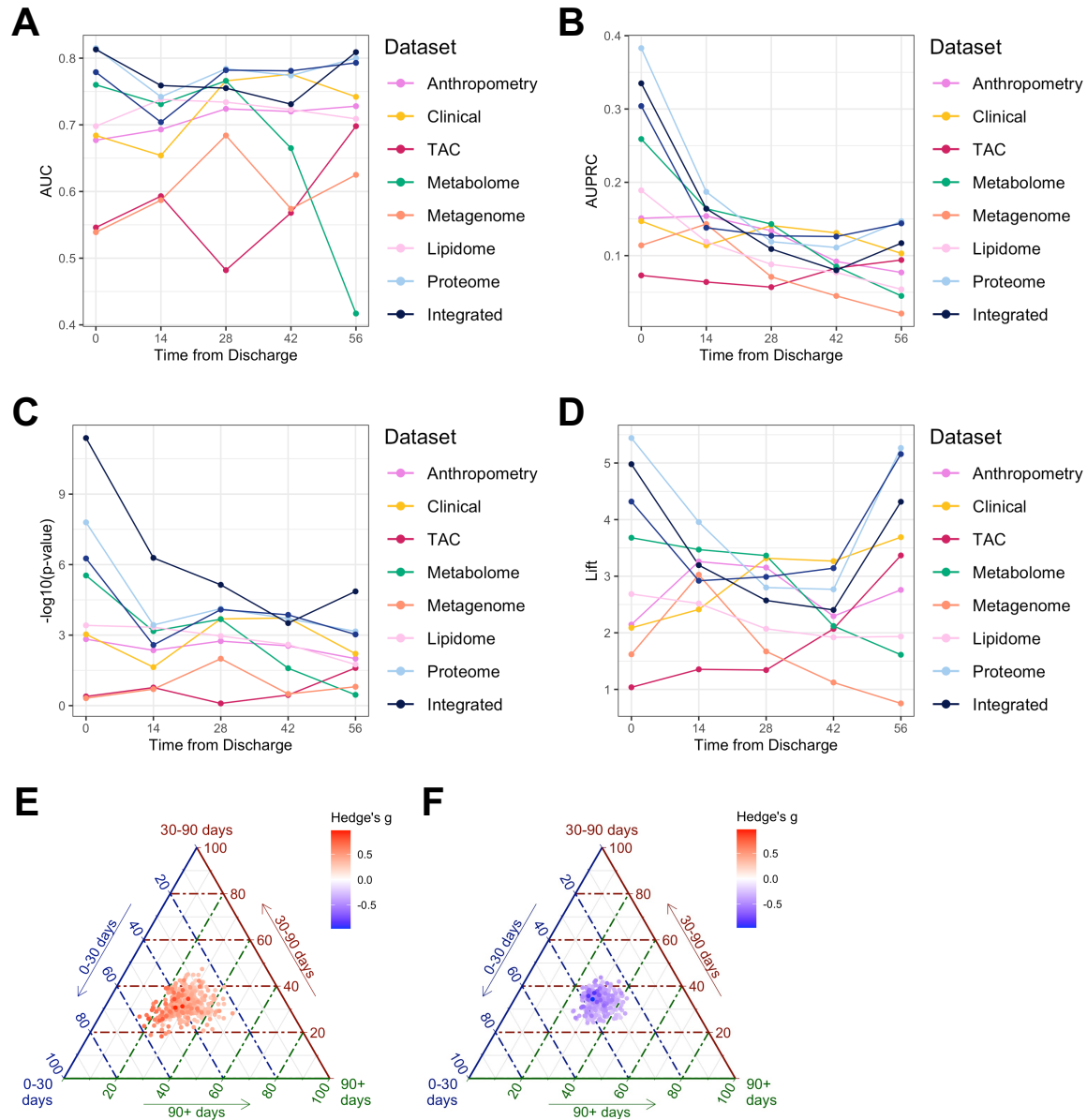


Figure S13. Temporal analysis of the multiomic signature of mortality in the post-discharge period. (A-D) Cross-validated XGBoost models were built using each dataset separately for the prediction of mortality in the post-discharge period and their performances assessed using only the cases that occurred in 14-day intervals. AUROCs (A), AUPRCs (B), unadjusted two-tailed Wilcoxon p-values (C), and lifts (prevalence-adjusted AUPRCs, D) of the models built on each dataset evaluated on 14-day intervals. (E-F) The hedge's g for each feature's association with mortality or survival at discharge was calculated using only cases that died in the specified timeframe. Ternary plots depicting each timeframe's relative hedge's g for each feature significantly associated with mortality (E) or survival (F) with at least a small effect size ($|\text{hedge's } g| > 0.2$).

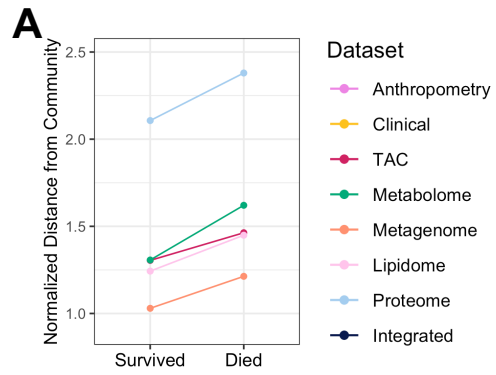


Figure S14. Multiomic diversity at discharge. (A) Median normalized distance from the community at discharge stratified by outcome for each omic dataset analyzed.

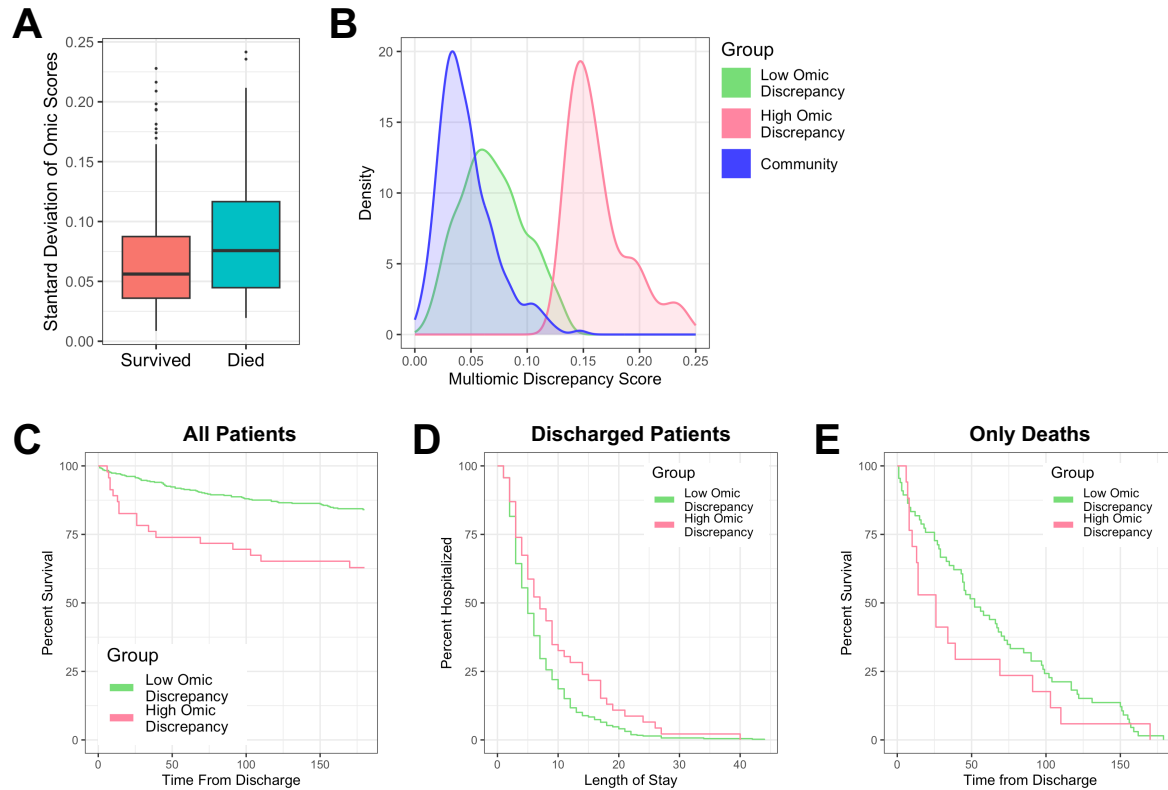


Figure S15. Characterization of the patient subgroups with discrepant interomic mortality risk scores at discharge. (A) Multiomic discrepancy scores of the models in **Figure 4B** stratified by patient outcome ($N = 466$). (B-E) Cross-validated XGBoost models for the prediction of mortality in the post-discharge period were trained on each omic dataset for the subset of discovery cohort members with all omics datasets available at discharge ($N = 466$). The risk scores of community members based on these models were then calculated. (B) Distribution of multiomic discrepancy scores, with colors representing patient subgroups. (C) Kaplan-Meier survival curves for the discrepant subgroups defined in **B** showing the survival curves based on all patients. (D) Kaplan-Meier curve for the discrepant subgroups defined in **B** showing the length of hospital stay for all discharged patients. (E) Kaplan-Meier survival curves for the discrepant subgroups defined in **B** showing the survival curve based on only patients that died. Box plots indicate median (middle line); 25th and 75th percentiles (box limits); 1.5*interquartile range (error bars); and outliers (single points).

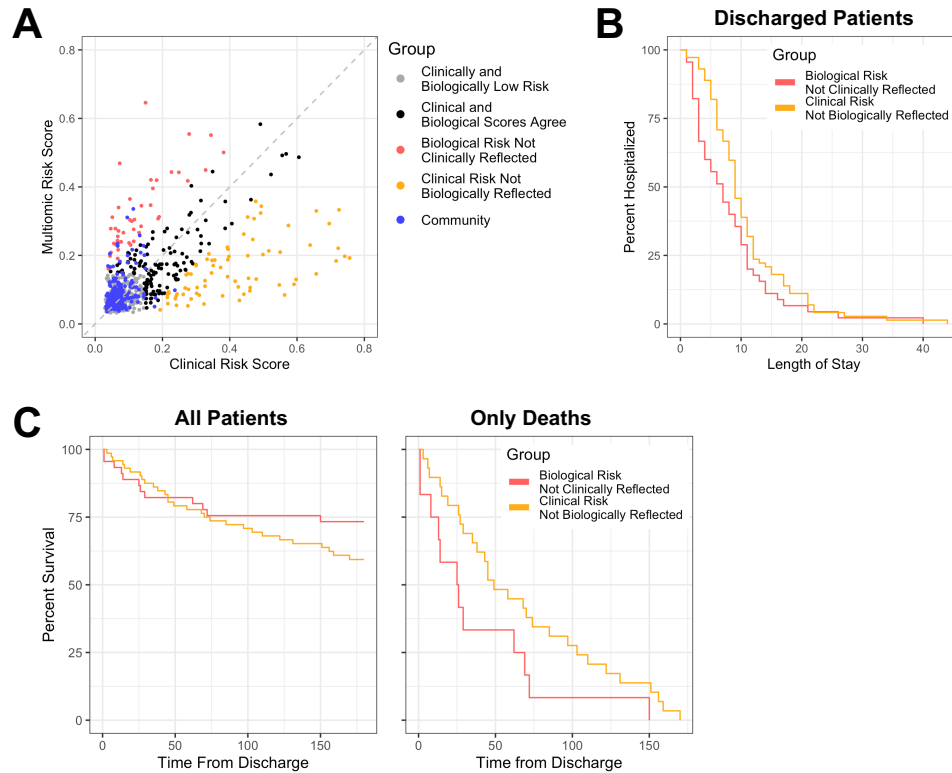


Figure S16. Contrastive analysis of the multiomic and clinical models of mortality at discharge. Cross-validated XGBoost models for the prediction of mortality in the post-discharge period were trained on the clinical data and the integrated multiomic data for the subset of discovery cohort members with all omics datasets available at discharge ($N = 466$). The risk scores of community members based on these models were then calculated. **(A)** Comparison between the mortality risk scores predicted by the multiomic and the clinical models, with colors representing patient subgroups. **(B)** Kaplan-Meier curve for the discrepant subgroups defined in **A** showing the length of hospital stay for all discharged patients. **(C)** Kaplan-Meier survival curves for the discrepant subgroups defined in **A** showing the survival curves based on all patients (left) or only on patients that died (right).

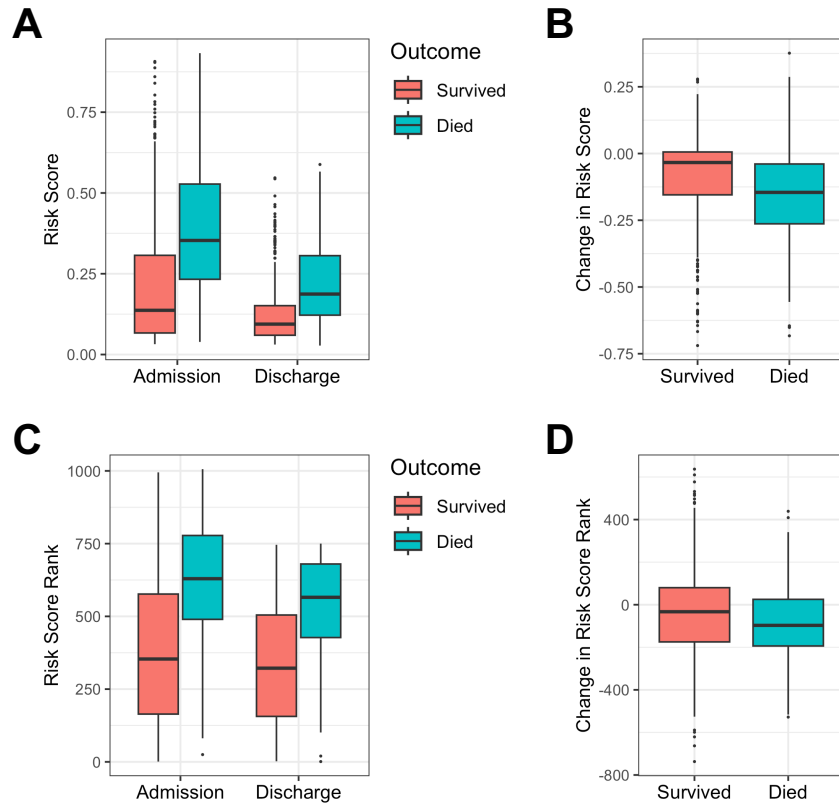


Figure S17. Comparison of the multiomic mortality risk scores between hospital admission and discharge. Cross-validated XGBoost models were built on the integrated multiomic data for the prediction of mortality during hospitalization or in the post-discharge period using data collected at hospital admission or for the prediction of mortality in the post-discharge period using data collected at discharge. **(A)** Multiomic mortality risk scores stratified by outcome and timepoint. **(B)** Change in multiomic mortality risk scores stratified by outcome. **(C)** Multiomic mortality risk score rank stratified by outcome and timepoint. **(D)** Change in multiomic mortality risk score rank stratified by outcome. Box plots indicate median (middle line); 25th and 75th percentiles (box limits); 1.5*interquartile range (error bars); and outliers (single points).

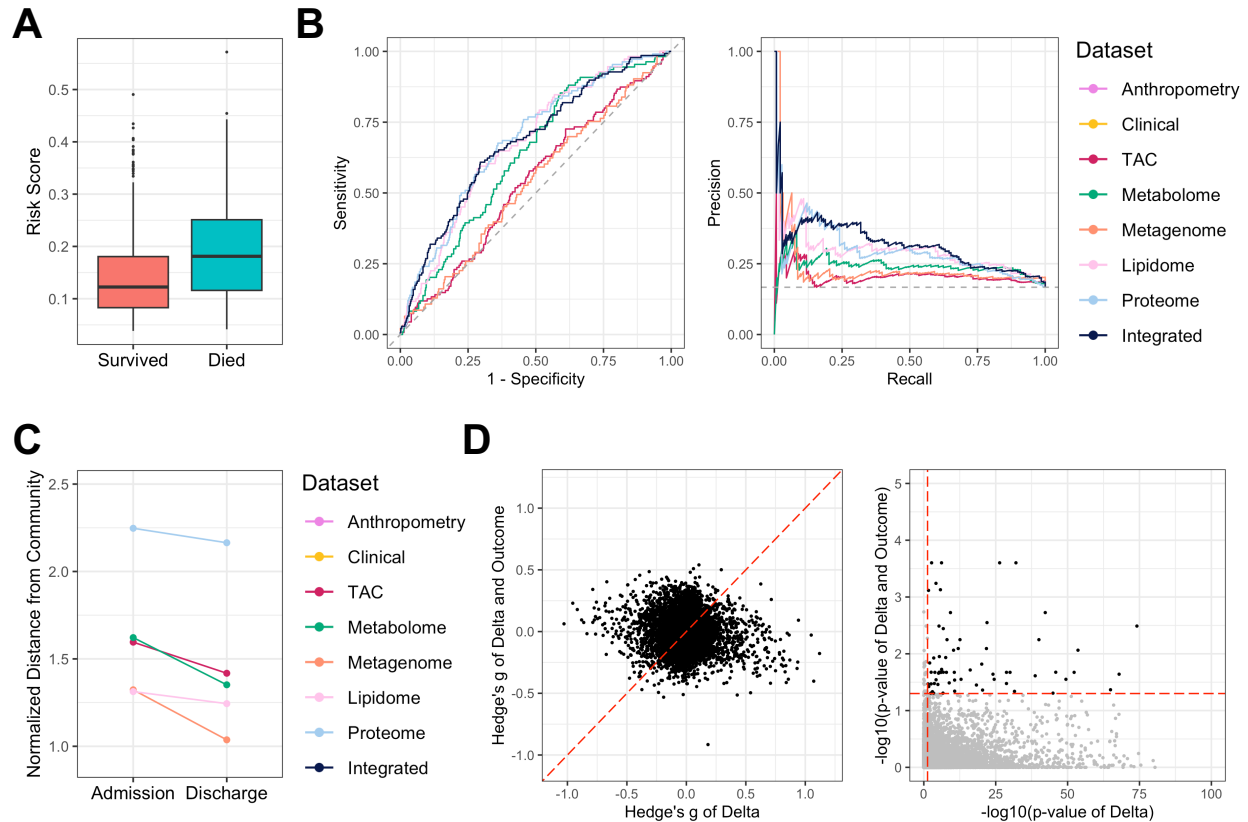


Figure S18. Impact of hospitalization on the multiomic signatures of mortality at discharge.

The change in each multiomic feature was calculated for all patients with data at both admission and discharge. An XGBoost model for the prediction of mortality in the post-discharge period was trained on the integrated multiomic change data. **(A)** Distribution of the mortality risk scores predicted by the multiomic change model stratified by patient outcome. **(B)** Cross-validated XGBoost models were built using each change dataset separately for the prediction of mortality in the post-discharge period. Left: Receiver-operating characteristic curves for the multiomic change model and the models built on each change dataset. Right: Precision-recall curve for the multiomic change model and the models built on each change dataset. **(C)** Median normalized distance from the community at hospital admission and discharge for each dataset analyzed. **(D)** Comparison of the change in multiomic features between admission and discharge and the association of this change to post-discharge mortality, assessed using effect size (Left) and FDR-adjusted statistical significance assessed using two-tailed Wilcoxon signed-rank test (Right). Box plots indicate median (middle line); 25th and 75th percentiles (box limits); 1.5*interquartile range (error bars); and outliers (single points).

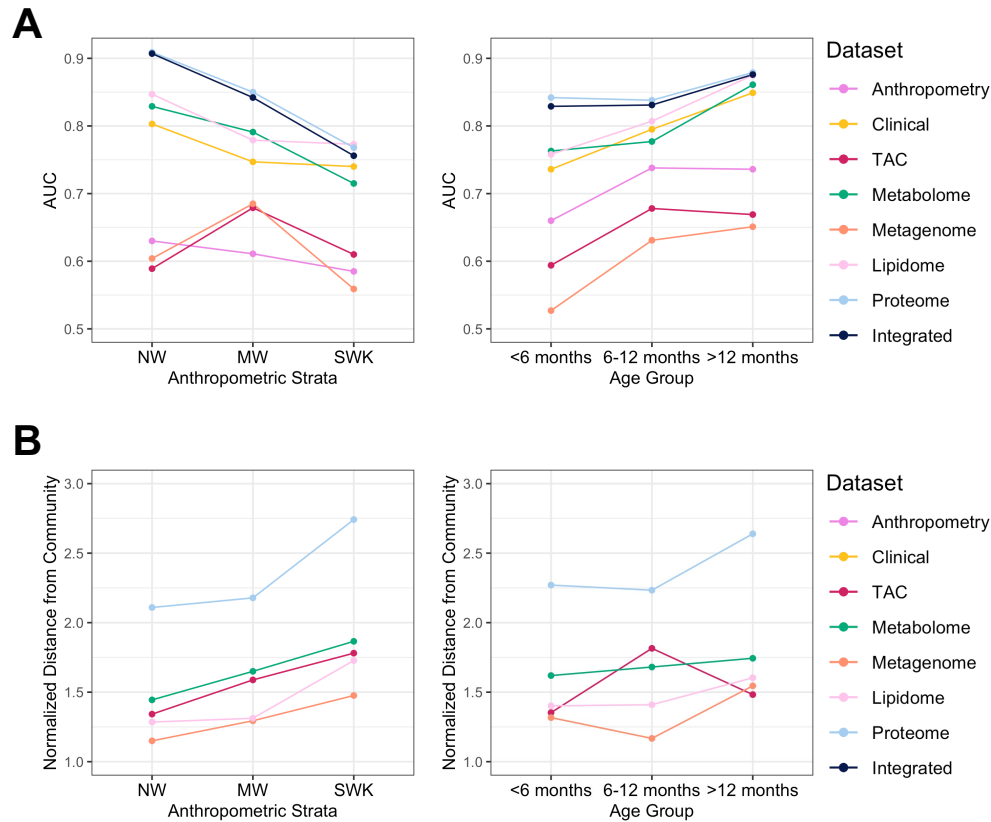


Figure S19. Characterizing the impact of anthropometric strata and age on the multiomic signature of mortality at hospital admission. Cross-validated XGBoost models for the prediction of mortality during hospitalization or in the post-discharge period of the discovery cohort were trained on the data collected at hospital admission. **(A)** Model performances stratified by anthropometric strata (left) and age group (right). **(B)** Median normalized distance from the community stratified by anthropometric strata and age group for each omic dataset analyzed and the integrated multiomic data. NW = Not Wasted, MW = Moderately Wasted, and SWK = Severely Wasted or Kwashiorkor.

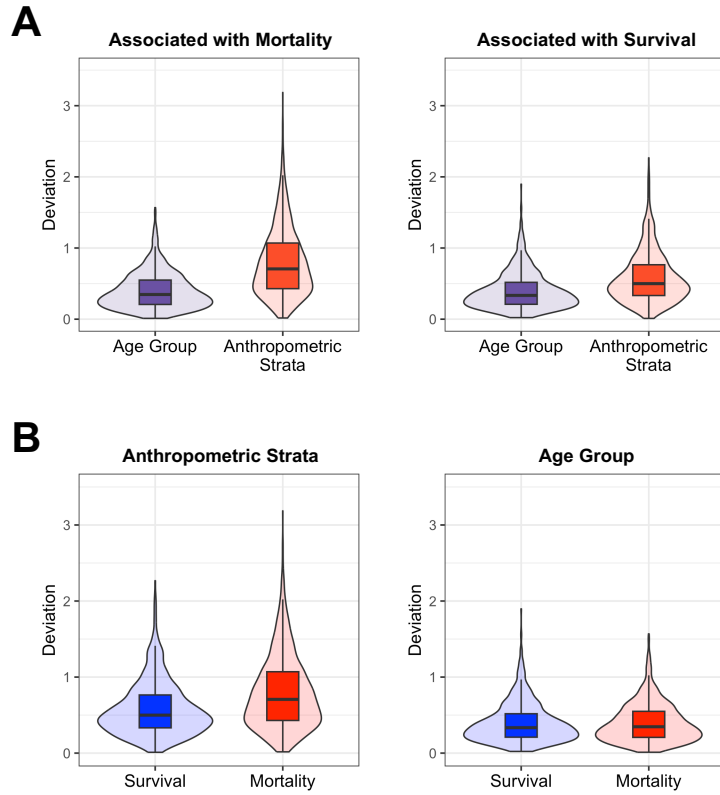


Figure S20. Feature associations with mortality and survival within anthropometric strata and age groups at hospital admission. Feature deviation scores within anthropometric strata and age groups were calculated at hospital admission for each feature significantly associated with mortality or survival with at least a small effect size ($|\text{hedge's } g| > 0.2$) (A) The distribution of feature deviation scores at hospital admission by association with mortality (left) or survival (right). (B) The distribution of feature deviation scores at hospital admission by anthropometric strata (left) and age group (right). Box plots indicate median (middle line); 25th and 75th percentiles (box limits); 1.5*interquartile range (error bars); and outliers (single points).

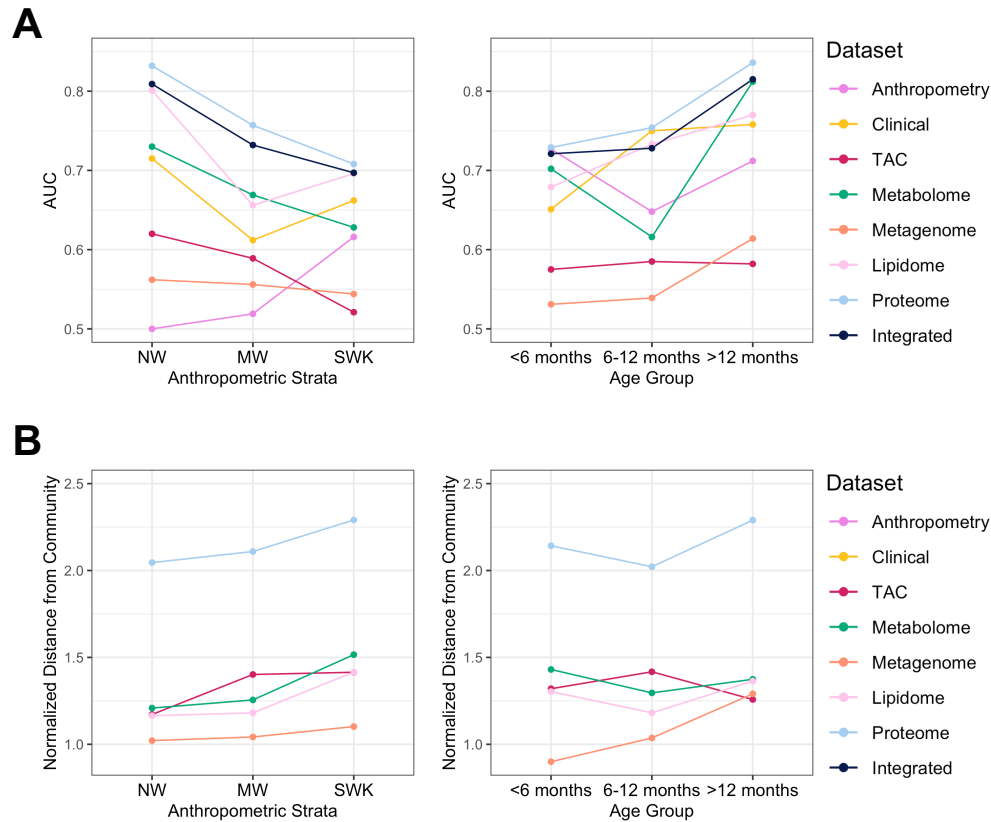


Figure S21. Characterizing the impact of anthropometric strata and age on the multiomic signature of mortality at discharge. Cross-validated XGBoost models for the prediction of mortality in the post-discharge period of the discovery cohort were trained on the data collected at discharge. **(A)** Model performances stratified by anthropometric strata (left) and age group (right). **(B)** Median normalized distance from the community stratified by anthropometric strata and age group for each omic dataset analyzed and the integrated multiomic data. NW = Not Wasted, MW = Moderately Wasted, and SWK = Severely Wasted or Kwashiorkor.

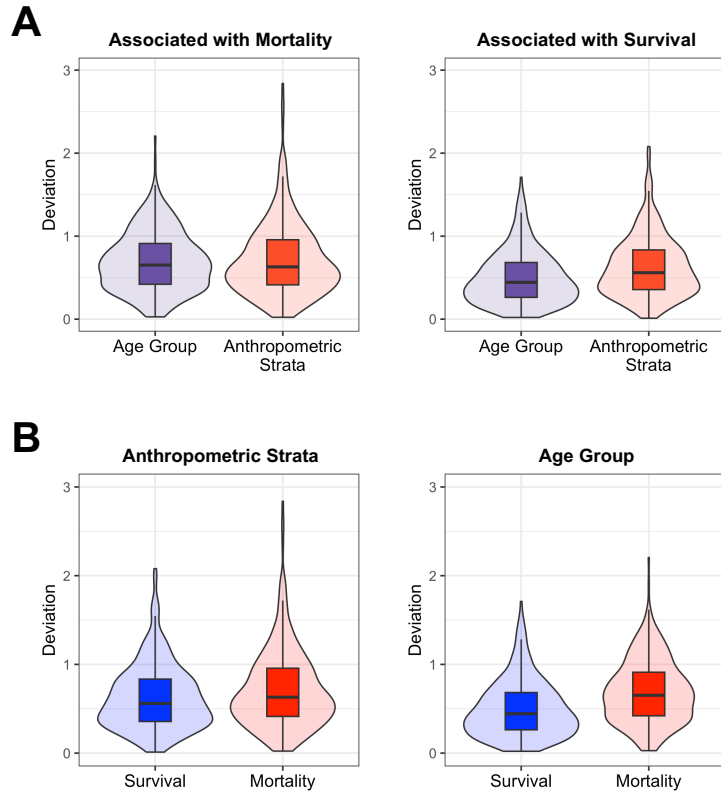


Figure S22. Feature associations with mortality and survival within anthropometric strata and age groups at discharge. Feature deviation scores within anthropometric strata and age groups were calculated at discharge for each feature significantly associated with mortality or survival with at least a small effect size ($|\text{hedge's } g| > 0.2$) (**A**) The distribution of feature deviation scores at discharge by association with mortality (left) or survival (right). (**B**) The distribution of feature deviation scores at discharge by anthropometric strata (left) and age group (right). Box plots indicate median (middle line); 25th and 75th percentiles (box limits); 1.5*interquartile range (error bars); and outliers (single points).

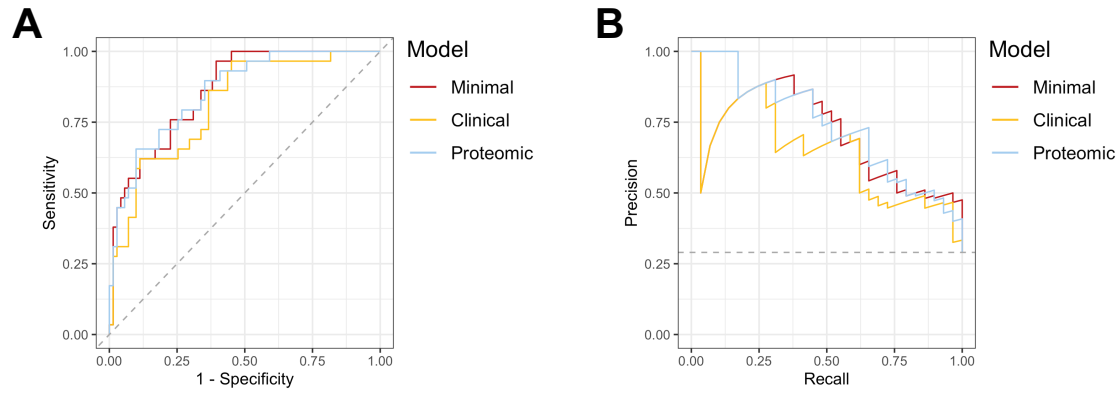


Figure S23. Performance on the validation cohort of the minimal model for the prediction of mortality during hospitalization and post-discharge. The minimal, proteomic, and clinical XGBoost model for the prediction of mortality trained on the discovery cohort were applied on the validation cohort. ROC (A) and precision-recall (B) curves for the minimal, proteomic, and clinical models.

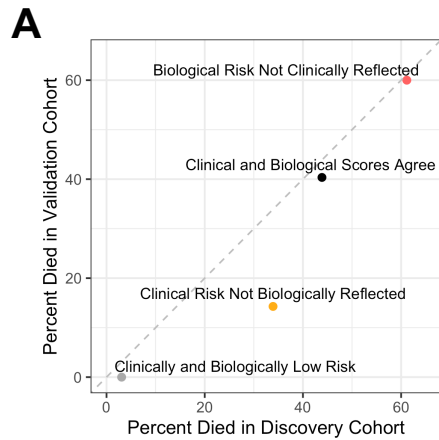


Figure S24. Characterization of the patient subgroups with discrepant clinical and multiomic mortality risk scores in the validation cohort. The cross-validated XGBoost models for the prediction of mortality during hospitalization or in the post-discharge period trained on the proteomics data and the clinical data of the discovery cohort were used to generate mortality risk scores for the validation cohort. **(A)** Comparison of subgroup percent mortality in the discovery cohort and the validation cohort for the patient subgroups defined in **Figure 3A** and **Figure 6G**.

A

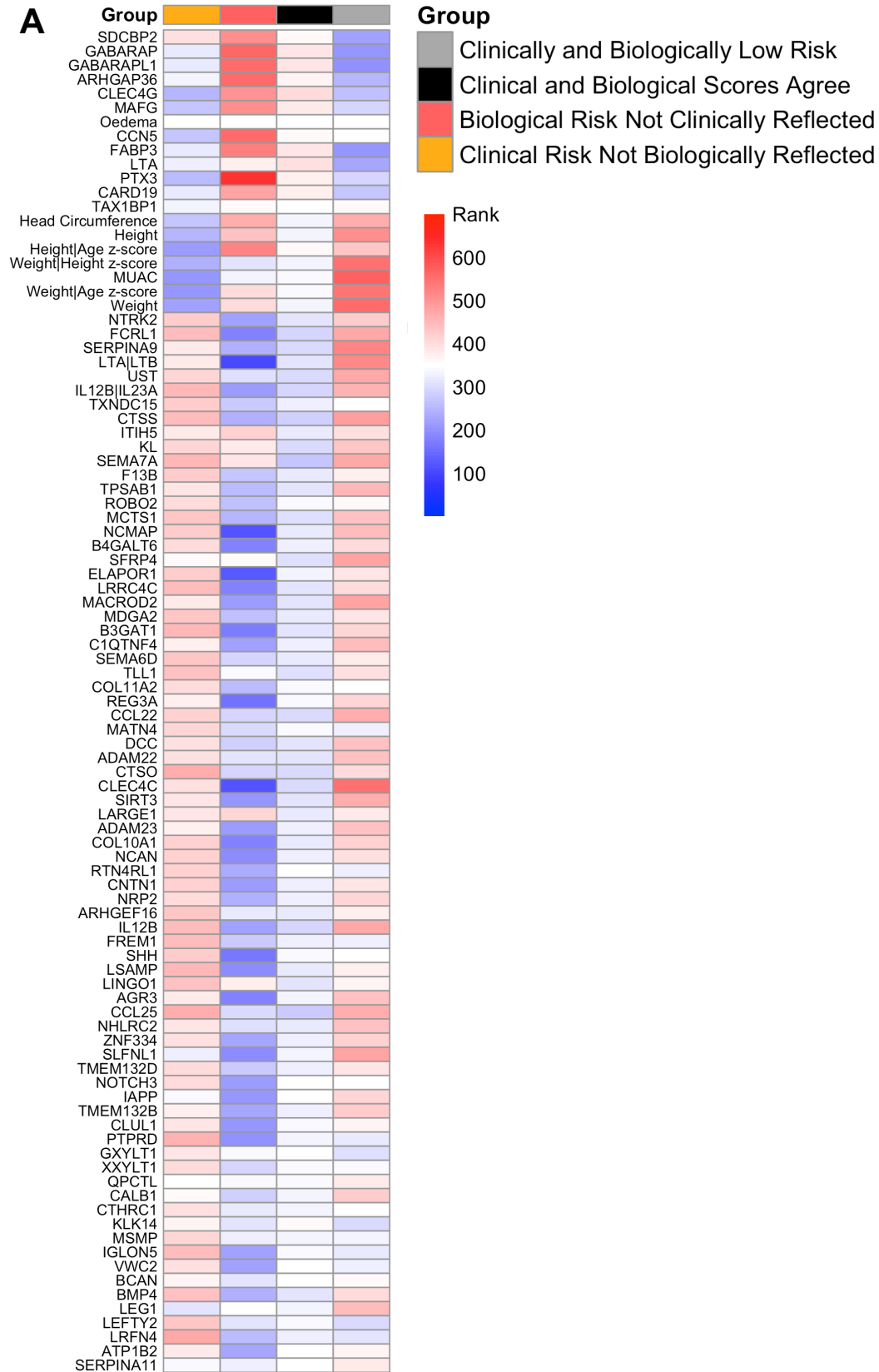


Figure S25. Contrasting features of the patient subgroups with discrepant clinical and multiomic mortality risk scores in the validation cohort. The cross-validated XGBoost models for the prediction of mortality during hospitalization or in the post-discharge period trained on the proteomics data and the clinical data of the discovery cohort were used to generate mortality risk scores for the validation cohort. (A) Heatmap of the clinical and multiomic features most different between the discrepant subgroups defined in **Figure 3A** assessed in the validation cohort.

Supplementary Tables

Table S1: Features driving the predictive power of the multiomic admissions model for the prediction of mortality during hospitalization and post-discharge.

Dataset	Feature	Name
Lipidome	TG_(58:10)	TG 58:10
Proteome	seq.10743.13	SLITRK1
Proteome	seq.13118.5	SMOC1
Proteome	seq.15295.81	IGF2
Proteome	seq.2571.12	IGFBP3
Proteome	seq.2952.75	IGF1
Proteome	seq.3291.30	FCER2
Proteome	seq.5437.63	FABP3
Proteome	seq.5728.60	FCRL1
Proteome	seq.9094.5	CLEC4C
Proteome	seq.4234.8	IL1RL1
Proteome	seq.8235.48	CHGB

Table S2: Performance statistics of the models at hospital admission built on each dataset for the prediction of mortality during hospitalization or in the post-discharge period. Significance was assessed using a two-sided Wilcoxon rank-sum test.

Dataset	<i>N</i>	AUROC [95% CI]	AUPRC [95% CI]	Wilcoxon <i>P</i>
Anthropometry	1001	0.73 [0.70, 0.76]	0.56 [0.51, 0.61]	2.5×10^{-32}
Clinical Variables	966	0.80 [0.77, 0.83]	0.70 [0.65, 0.74]	3.6×10^{-51}
TAC	993	0.66 [0.63, 0.70]	0.50 [0.46, 0.55]	6.5×10^{-17}
Metabolome	924	0.80 [0.77, 0.83]	0.69 [0.64, 0.73]	6.0×10^{-51}
Metagenome	757	0.62 [0.57, 0.66]	0.46 [0.41, 0.51]	1.7×10^{-7}
Lipidome	906	0.82 [0.79, 0.85]	0.69 [0.64, 0.74]	3.8×10^{-55}
Proteome	945	0.85 [0.83, 0.88]	0.76 [0.72, 0.80]	1.8×10^{-69}
Multiomic Integrated	1007	0.84 [0.82, 0.87]	0.75 [0.71, 0.79]	6.7×10^{-72}

Table S3: Performance statistics of the multiomic model at hospital admission for the prediction of mortality during hospitalization or in the post-discharge period stratified by study site. Significance was assessed using a two-sided Wilcoxon rank-sum test.

Study Site	<i>N</i>	Percent Died	AUROC [95% CI]	AUPRC [95% CI]	Wilcoxon <i>P</i>
Banfora	141	39.0%	0.80 [0.72, 0.87]	0.75 [0.65, 0.85]	3.0*10 ⁻⁹
Blantyre	113	34.5%	0.86 [0.78, 0.93]	0.76 [0.64, 0.88]	5.2*10 ⁻¹⁰
Dhaka	108	18.5%	0.81 [0.71, 0.92]	0.51 [0.33, 0.71]	1.3*10 ⁻⁵
Kampala	155	34.2%	0.79 [0.71, 0.86]	0.67 [0.56, 0.80]	5.4*10 ⁻⁹
Karachi	110	32.7%	0.79 [0.70, 0.87]	0.66 [0.53, 0.78]	1.2*10 ⁻⁶
Kilifi	74	29.7%	0.93 [0.88, 0.99]	0.86 [0.74, 0.95]	5.0*10 ⁻⁹
Matlab	79	8.9%	0.85 [0.62, 1.00]	0.71 [0.40, 0.98]	2.6*10 ⁻³
Mbagathi	102	44.1%	0.78 [0.69, 0.87]	0.78 [0.68, 0.86]	1.2*10 ⁻⁶
Migori	125	58.4%	0.81 [0.74, 0.89]	0.85 [0.77, 0.91]	2.6*10 ⁻⁹

Table S4: Features of the minimal admissions model for the prediction of mortality during hospitalization and post-discharge.

Dataset	Feature	Name
Lipidome	TG_(58:10)	TG 58:10
Proteome	seq.10743.13	SLITRK1
Proteome	seq.13118.5	SMOC1
Proteome	seq.22560.1	EVI2A
Proteome	seq.2571.12	IGFBP3
Proteome	seq.3069.52	IGHM
Proteome	seq.3505.6	LTA LTB
Proteome	seq.5437.63	FABP3
Proteome	seq.5728.60	FCRL1
Proteome	seq.9094.5	CLEC4C

Table S5: Features of the minimal admissions model for the classification of patients into discrepant subgroups.

Dataset	Feature	Name
Lipidome	PE_(40:7)	PE 40:7
Proteome	seq.10435.2	AGA
Proteome	seq.13618.15	MAD1L1
Proteome	seq.15653.9	COL10A1
Proteome	seq.22985.160	IGFBP2
Proteome	seq.23591.9	EXD1
Proteome	seq.25960.15	PLS3
Proteome	seq.5699.19	FAM189A2
Proteome	seq.6383.90	TLL1
Proteome	seq.9185.15	TFF1

Table S6: Performance statistics of the models built on each dataset at discharge for the prediction of mortality in the post-discharge period. Significance was assessed using a two-sided Wilcoxon rank-sum test.

Dataset	<i>N</i>	AUROC [95% CI]	AUPRC [95% CI]	Wilcoxon <i>P</i>
Anthropometry	825	0.70 [0.66, 0.75]	0.40 [0.34, 0.47]	3.2×10^{-16}
Clinical Variables	802	0.72 [0.68, 0.77]	0.40 [0.34, 0.47]	1.6×10^{-18}
TAC	739	0.58 [0.53, 0.64]	0.24 [0.20, 0.30]	0.003
Metabolome	648	0.70 [0.64, 0.75]	0.37 [0.30, 0.46]	3.2×10^{-11}
Metagenome	575	0.53 [0.47, 0.59]	0.21 [0.17, 0.26]	0.34
Lipidome	657	0.73 [0.68, 0.78]	0.37 [0.31, 0.45]	3.6×10^{-15}
Proteome	681	0.78 [0.73, 0.82]	0.44 [0.37, 0.53]	1.9×10^{-21}
Multiomic Integrated	750	0.77 [0.72, 0.81]	0.44 [0.37, 0.51]	1.5×10^{-22}

Table S7: Performance statistics of the multiomic model at discharge for the prediction of mortality in the post-discharge period stratified by study site. Significance was assessed using a two-sided Wilcoxon rank-sum test.

Study Site	<i>N</i>	Percent Died	AUROC [95% CI]	AUPRC [95% CI]	Wilcoxon <i>P</i>
Banfora	103	19.4%	0.67 [0.54, 0.80]	0.31 [0.21, 0.51]	0.02
Blantyre	74	21.6%	0.81 [0.70, 0.91]	0.56 [0.37, 0.75]	2.1*10 ⁻⁴
Dhaka	99	11.1%	0.77 [0.60, 0.94]	0.33 [0.16, 0.58]	0.004
Kampala	108	13.0%	0.70 [0.56, 0.83]	0.33 [0.15, 0.57]	0.02
Karachi	85	27.1%	0.73 [0.61, 0.86]	0.58 [0.41, 0.74]	0.001
Kilifi	58	15.5%	0.81 [0.68, 0.94]	0.46 [0.23, 0.76]	0.002
Matlab	74	5.4%	0.97 [0.91, 1.00]	0.75 [0.34, 1.00]	0.002
Mbagathi	75	26.7%	0.75 [0.61, 0.89]	0.57 [0.38, 0.78]	0.001
Migori	74	31.1%	0.60 [0.47, 0.74]	0.36 [0.28, 0.54]	0.16

Table S8: Normalized omic distance comparisons between anthropometric strata and age groups at hospital admission. Significance was assessed using a two-sided Wilcoxon rank-sum test. Dataset and comparisons not present did not achieve FDR-corrected statistical significance. NW = Not Wasted, MW = Moderately Wasted, and SWK = Severely Wasted or Kwashiorkor. FDR = False Discovery Rate.

Dataset	Groups Compared		FDR-corrected Wilcoxon <i>P</i>
TAC	<6 months	6-12 months	0.001
Metagenome	6-12 months	>12 months	0.02
Lipidome	6-12 months	>12 months	0.01
Proteome	<6 months	>12 months	0.02
TAC	NW	MW	0.03
TAC	NW	SWK	5.3×10^{-4}
Metabolome	NW	SWK	4.6×10^{-7}
Metabolome	MW	SWK	0.01
Lipidome	NW	SWK	4.6×10^{-7}
Lipidome	MW	SWK	6.5×10^{-6}
Proteome	NW	SWK	1.4×10^{-6}
Proteome	MW	SWK	1.9×10^{-4}

Table S9: Normalized omic distance comparisons between anthropometric strata and age groups at discharge. Significance was assessed using a two-sided Wilcoxon rank-sum test. Dataset and comparisons not present did not achieve FDR-corrected statistical significance. NW = Not Wasted, MW = Moderately Wasted, and SWK = Severely Wasted or Kwashiorkor. FDR = False Discovery Rate.

Dataset	Groups Compared		FDR-corrected Wilcoxon <i>P</i>
Metagenome	<6 months	6-12 months	0.03
Metagenome	<6 months	>12 months	4.0×10^{-5}
Metagenome	6-12 months	>12 months	0.03
Metabolome	NW	SWK	2.8×10^{-9}
Metabolome	MW	SWK	1.4×10^{-5}
Lipidome	NW	SWK	9.2×10^{-4}
Lipidome	MW	SWK	0.005
Proteome	NW	SWK	0.007

Table S10: Features of the minimal model for the prediction of mortality on the validation cohort.

Dataset	Feature	Name
Proteome	seq.10743.13	SLITRK1
Proteome	seq.10781.19	CLEC4G
Proteome	seq.13118.5	SMOC1
Proteome	seq.15295.81	IGF2
Proteome	seq.2571.12	IGFBP3
Proteome	seq.2952.75	IGF1
Proteome	seq.4234.8	IL1RL1
Proteome	seq.5437.63	FABP3
Proteome	seq.5728.60	FCRL1
Proteome	seq.6557.50	LRRC15

Table S11: Features of the minimal model for the classification of patients into discrepant subgroups in the validation cohort.

Dataset	Feature	Name
Proteome	seq.13104.32	EFNB1
Proteome	seq.13658.31	PDGFC
Proteome	seq.13979.3	SLC26A7
Proteome	seq.16919.1	DBI
Proteome	seq.23632.22	SLFNL1
Proteome	seq.3505.6	LTA LTB
Proteome	seq.7266.4	SERPINA9
Proteome	seq.8445.184	MELT
Proteome	seq.9094.5	CLEC4C